

## SEQUENCE LISTING

<110> Keith, Jr., James C.  
McCoy, John M.  
Mi, Sha

<120> Methods and compositions for diagnosing  
and treating preeclampsia and gestational trophoblast  
disorders

<130> GIN-6006B4

<150> 60/216,657  
<151> 2000-07-06

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 2930  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (930)...(2546)

<400> 1  
aatcggtctg cttatcgcc aagtccttc aggagaacaa agaacaggcc attaccctgg 60  
agaagactgg caactgattt taccacaag cccaaacctc agggatttca gtatctacta 120  
gtctggtag atacttcac gggttggca gggccttcc cctgttaggac agaaaaggcc 180  
caagaggtaa taaaggcact agttcatgaa ataattccca gattcggact tccccgaggc 240  
ttacagagtg acaatagccc tgctttccag gccacagtaa cccaggagat atcccaggcg 300  
ttaggtatac gatatactt acactgcgcc tgaaggccac agtcctcagg gaaggtcgag 360  
aaaatgaatg aaacactcaa agacatcta aaaaagcaaa cccaggaaac ccacctcaca 420  
tgccctgctc tggccttat agccttaaaa agaatctgca actttccccca aaaagcagga 480  
cttagcccat acgaaatgct gtatgaaagg cccttcataa ccaatgaccc tggcttgac 540  
ccaagacagc caacttagtt gcagacatca cctccttagc caaatatcaa caagttctta 600  
aaacattaca aggaacctat ccctgagaag agggaaaaga actattccac ccttgtgaca 660  
tggatttagt caagtccctt ccctctaatt cccatccct agatacatcc tggaaaggac 720  
ccatccctgtt accccaactg cggttaaagt ggctggagtg gagtcttgg 780  
tacatcacac ttgagtcaaa tccctggatac tgccaaagga acctgaaaat ccaggagaca 840  
acgctagcta ttccctgtgaa ccctcttaggg atttgcgcct gctcttcaaa caacaaccag 900  
gaggaaagta actaaaatca taaatcccc atg gcc ctc cct tat cat att ttt 953

Met Ala Leu Pro Tyr His Ile Phe  
1 5

ctc ttt act gtt ctt tta ccc tct ttc act ctc act gca ccc cct cca 1001  
Leu Phe Thr Val Leu Leu Pro Ser Phe Thr Leu Thr Ala Pro Pro Pro  
10 15 20

tgc cgc tgt atg acc agt agc tcc cct tac caa gag ttt cta tgg aga 1049  
Cys Arg Cys Met Thr Ser Ser Pro Tyr Gln Glu Phe Leu Trp Arg  
25 30 35 40

atg cag cgt ccc gga aat att gat gcc cca tcg tat agg agt ctt tct 1097  
Met Gln Arg Pro Gly Asn Ile Asp Ala Pro Ser Tyr Arg Ser Leu Ser  
45 50 55

aag gga acc ccc acc ttc act gcc cac acc cat atg ccc cgc aac tgc Lys Gly Thr Pro Thr Phe Thr Ala His Thr His Met Pro Arg Asn Cys 60 65 70	1145
tat cac tct gcc act ctt tgc atg cat gca aat act cat tat tgg aca Tyr His Ser Ala Thr Leu Cys Met His Ala Asn Thr His Tyr Trp Thr 75 80 85	1193
gga aaa atg att aat cct agt tgt cct gga gga ctt gga gtc act gtc Gly Lys Met Ile Asn Pro Ser Cys Pro Gly Gly Leu Gly Val Thr Val 90 95 100	1241
tgt tgg act tac ttc acc caa act ggt atg tct gat ggg ggt gga gtt Cys Trp Thr Tyr Phe Thr Gln Thr Gly Met Ser Asp Gly Gly Val 105 110 115 120	1289
caa gat cag gca aga gaa aaa cat gta aaa gaa gta atc tcc caa ctc Gln Asp Gln Ala Arg Glu Lys His Val Lys Glu Val Ile Ser Gln Leu 125 130 135	1337
acc cgg gta cat ggc acc tct agc ccc tac aaa gga cta gat ctc tca Thr Arg Val His Gly Thr Ser Ser Pro Tyr Lys Gly Leu Asp Leu Ser 140 145 150	1385
aaa cta cat gaa acc ctc cgt acc cat act cgc ctg gta agc cta ttt Lys Leu His Glu Thr Leu Arg Thr His Thr Arg Leu Val Ser Leu Phe 155 160 165	1433
aat acc acc ctc act ggg ctc cat gag gtc tcg gcc caa aac cct act Asn Thr Thr Leu Thr Gly Leu His Glu Val Ser Ala Gln Asn Pro Thr 170 175 180	1481
aac tgt tgg ata tgc ctc ccc ctg aac ttc agg cca tat gtt tca atc Asn Cys Trp Ile Cys Leu Pro Leu Asn Phe Arg Pro Tyr Val Ser Ile 185 190 195 200	1529
cct gta cct gaa caa tgg aac aac ttc agc aca gaa ata aac acc act Pro Val Pro Glu Gln Trp Asn Asn Phe Ser Thr Glu Ile Asn Thr Thr 205 210 215	1577
tcc gtt tta gta gga cct ctt gtt tcc aat ctg gaa ata acc cat acc Ser Val Leu Val Gly Pro Leu Val Ser Asn Leu Glu Ile Thr His Thr 220 225 230	1625
tca aac ctc acc tgt gta aaa ttt agc aat act aca tac aca acc aac Ser Asn Leu Thr Cys Val Lys Phe Ser Asn Thr Thr Tyr Thr Asn 235 240 245	1673
tcc caa tgc atc agg tgg gta act cct ccc aca caa ata gtc tgc cta Ser Gln Cys Ile Arg Trp Val Thr Pro Pro Thr Gln Ile Val Cys Leu 250 255 260	1721
ccc tca gga ata ttt ttt gtc tgt ggt acc tca gcc tat cgt tgt ttg Pro Ser Gly Ile Phe Phe Val Cys Gly Thr Ser Ala Tyr Arg Cys Leu 265 270 275 280	1769
aat ggc tct tca gaa tct atg tgc ttc ctc tca ttc tta gtg ccc cct Asn Gly Ser Ser Glu Ser Met Cys Phe Leu Ser Phe Leu Val Pro Pro 285 290 295	1817

atg acc atc tac act gaa caa gat tta tac aat tat gtc ata tct aag Met Thr Ile Tyr Thr Glu Gln Asp Leu Tyr Asn Tyr Val Ile Ser Lys 300 305 310	1865
ccc cgc aac aaa aga gta ccc att ctt cct ttt gtt ata gga gca gga Pro Arg Asn Lys Arg Val Pro Ile Leu Pro Phe Val Ile Gly Ala Gly 315 320 325	1913
gtg cta ggt gca cta ggt act ggc att ggc ggt atc aca acc tct act Val Leu Gly Ala Leu Gly Thr Gly Ile Gly Gly Ile Thr Thr Ser Thr 330 335 340	1961
cag ttc tac tac aaa cta tct caa gaa cta aat ggg gac atg gaa cgg Gln Phe Tyr Tyr Lys Leu Ser Gln Glu Leu Asn Gly Asp Met Glu Arg 345 350 355 360	2009
gtc gcc gac tcc ctg gtc acc ttg caa gat caa ctt aac tcc cta gca Val Ala Asp Ser Leu Val Thr Leu Gln Asp Gln Leu Asn Ser Leu Ala 365 370 375	2057
gca gta gtc ctt caa aat cga aga gct tta gac ttg cta acc gct gaa Ala Val Val Leu Gln Asn Arg Arg Ala Leu Asp Leu Leu Thr Ala Glu 380 385 390	2105
aga ggg gga acc tgt tta ttt tta ggg gaa gaa tgc tgt tat tat gtt Arg Gly Gly Thr Cys Leu Phe Leu Gly Glu Glu Cys Cys Tyr Tyr Val 395 400 405	2153
aat caa tcc gga atc gtc act gag aaa gtt aaa gaa att cga gat cga Asn Gln Ser Gly Ile Val Thr Glu Lys Val Lys Glu Ile Arg Asp Arg 410 415 420	2201
ata caa cgt aga gca gag gag ctt cga aac act gga ccc tgg ggc ctc Ile Gln Arg Arg Ala Glu Glu Leu Arg Asn Thr Gly Pro Trp Gly Leu 425 430 435 440	2249
ctc agc caa tgg atg ccc tgg att ctc ccc ttc tta gga cct cta gca Leu Ser Gln Trp Met Pro Trp Ile Leu Pro Phe Leu Gly Pro Leu Ala 445 450 455	2297
gct ata ata ttg cta ctc ctc ttt gga ccc tgt atc ttt aac ctc ctt Ala Ile Ile Leu Leu Leu Phe Gly Pro Cys Ile Phe Asn Leu Leu 460 465 470	2345
gtt aac ttt gtc tct tcc aga atc gaa gct gta aaa cta caa atg gag Val Asn Phe Val Ser Ser Arg Ile Glu Ala Val Lys Leu Gln Met Glu 475 480 485	2393
ccc aag atg cag tcc aag act aag atc tac cgc aga ccc ctg gac cgg Pro Lys Met Gln Ser Lys Thr Lys Ile Tyr Arg Arg Pro Leu Asp Arg 490 495 500	2441
cct gct agc cca cga tct gat gtt aat gac atc aaa ggc acc cct cct Pro Ala Ser Pro Arg Ser Asp Val Asn Asp Ile Lys Gly Thr Pro Pro 505 510 515 520	2489
gag gaa atc tca gct gca caa cct cta cta cgc ccc aat tca gca gga Glu Glu Ile Ser Ala Ala Gln Pro Leu Leu Arg Pro Asn Ser Ala Gly 525 530 535	2537

agc agt tag agcggtcgtc ggccaacctc cccaaacagca cttaggaaaa 2586  
 Ser Ser \*

cctgttgaga tgggggactg agagacagga ctagctggat ttccctaggct gactaagaat 2646  
 ccctaaggcct agctggaaag gtgaccacat ccaccttaa acacggggct tgcaacttag 2706  
 ctcacacactg accaatcaga gagctcaact aaatgtaat taggcaaaaa caggaggtaa 2766  
 agaaatagcc aatcatctat tgcctgagag cacagcagga gggacaatga tcggatata 2826  
 aacccaagtgc ttcgagccgg caacggcaac ccccttggg tcccctccct ttgtatggg 2886  
 gctctgtttt catgctattt cactctatta aatcttgcaa ctgc 2930

<210> 2  
<211> 538  
<212> PRT  
<213> Homo sapiens

<400> 2  
 Met Ala Leu Pro Tyr His Ile Phe Leu Phe Thr Val Leu Leu Pro Ser  
 1 5 10 15  
 Phe Thr Leu Thr Ala Pro Pro Cys Arg Cys Met Thr Ser Ser Ser  
 20 25 30  
 Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp  
 35 40 45  
 Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala  
 50 55 60  
 His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met  
 65 70 75 80  
 His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys  
 85 90 95  
 Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr  
 100 105 110  
 Gly Met Ser Asp Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His  
 115 120 125  
 Val Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser  
 130 135 140  
 Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr  
 145 150 155 160  
 His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His  
 165 170 175  
 Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu  
 180 185 190  
 Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn  
 195 200 205  
 Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val  
 210 215 220  
 Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe  
 225 230 235 240  
 Ser Asn Thr Thr Tyr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr  
 245 250 255  
 Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys  
 260 265 270  
 Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys  
 275 280 285  
 Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp  
 290 295 300  
 Leu Tyr Asn Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile  
 305 310 315 320  
 Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly  
 325 330 335  
 Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln  
 340 345 350

Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu  
 355 360 365  
 Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Gln Asn Arg Arg  
 370 375 380  
 Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu  
 385 390 395 400  
 Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu  
 405 410 415  
 Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu  
 420 425 430  
 Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile  
 435 440 445  
 Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Phe  
 450 455 460  
 Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile  
 465 470 475 480  
 Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys  
 485 490 495  
 Ile Tyr Arg Arg Pro Leu Asp Arg Pro Ala Ser Pro Arg Ser Asp Val  
 500 505 510  
 Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro  
 515 520 525  
 Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser  
 530 535

<210> 3  
 <211> 20  
 <212> DNA  
 <213> Homo sapiens

<400> 3  
 cacaaccaac tcccaatgca

20

<210> 4  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens

<400> 4  
 agagccattc aaacaacgat agg

23

<210> 5  
 <211> 30  
 <212> DNA  
 <213> Homo sapiens

<400> 5  
 ctccctccac acaaatacgtc tgcctaccct

30